

Peck Farm Research Report Phase 4

Title: Comparing Bacterial Characteristics' of Whitetail Deer /Elk under CWD Quarantine

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Hypothesis: A Cervid supported with optimized feed, forage and water along with its genetics can stave off an initial or continuing disease process that could lead to the onset of a disease process like a neuro-degenerative disease called Chronic Wasting Disease (CWD).

Report delayed due to lab results timeline delay of normal processing due to Covid-19.

Wisconsin Commercial Deer and Elk Farmers Association (WCDEFA), North American Deer Farmers Association (NADeFA) , Deer Breeders Corporation (DBC) and Agricultural Omega Solutions LLC have continued to collectively fund this research investigation into the understanding of an initial disease process based on nutrition or lack of nutrition and negative associated environmental factors. This continuing investigation will help the members of the Captive Cervid Associations as well as other Wildlife Agencies in understanding the compounding environmental factors. These environmental factors, including water and feed support, if left unmanaged, can contribute to a pathogen bio-burden. This leads to an increased risk of disease including progressive neurodegenerative onset and subsequent mortality of cervids involving a detectable Chronic Wasting Disease.

Our test farm continues to exist under quarantine conditions in a CWD endemic area. At the same time, the wild deer population increases in CWD detection at post mortem examination.

This Phase 4 Research report utilizes past research data as a foundation in a continued effort to build upon the understanding that environmental organisms are causal to the degradation of deer's immunity. This pathway leads to identification of the neurodegenerative disease called CWD and how develops to a clinical case resulting in a positive detection or death in cervids. To review all past reports of this research, please visit WCDEFA wcdefa@gmail.com, NADeFA schafer@nadefa.org or DBC cati@dbcdeer.com.

Background

From the inception of this research project past and current findings were helpful in determining the current course and of future proposed research. Positive refinements and improvements include sample collection type and testing pathways. These refinements will help in expediting detection of negative environmental organisms (impacting health / disease status) and, more importantly, identify potential intervention strategies for any deer / elk in this study.

Phase 4 will seek to continue following the evolving health status of the remaining 3 deer on the quarantined farm (2 bucks, 1 Doe). New to this Phase of the study will be 1 bull elk that resides on this farm under quarantine but considered medically separated. Since only Does on the

quarantined farm have died from negative health conditions, 1 Doe from each control farm will be continued to be followed in this study for tracking both sexes in comparing deer health status.

As we continue to investigate live deer under quarantined conditions (4 + years time), it is important ,once identified, to understand how any disease process begins in deer before one is able to potentially counter these health complications moving forward.

Sampling of Deer

Each deer and 1 elk were tranquilized using the “Clear Dart” with MK package donated and delivered by Orion Whitetails for all animals in this study. All samples will be collected by an approved veterinarian licensed for approved services on the quarantine farm.

Since the deer and elk on the quarantine farm looked in good shape at the time of sampling they did not show any of the outward classical signs of being positive with CWD. In past observations, deer detected as rectal positives took a longer time to see their respective hair coat changes to the typical summer coat color or summer coat to winter coat. This was noticed more in rectal CWD positive deer as compared to the non- detected CWD deer. This lack of hair coat change could be attributed to the stage of disease the deer may experience.

This winter / spring there was one noticeable exception to the hair coat this year of Purple 1. She had developed Deer hair loss syndrome (DHLS) (1) over the winter which is of unknown origin. Once sedated, it was determined to be a hair coat condition caused by lice. This was rectified by using an anti louse / tick pour on product called dectomax rubbing it in along the neck down the back to the rump of the deer.

Keeping with past practices in this study, we only collect samples from the deer/ elk n the early spring of the year. This time of year is considered to have a lower environmental bacterial content and gives us w starting point when monitoring the health status through the winter season. This year with 3 deer left on the quarantined farm (Buck Red 1, Purple 1 and Purple 2) we proceeded in early April 2020 to collect samples of blood, nasal, saliva, and feces from these 3 deer and 1 bull elk. Rectal samplings were unavailable since 4 previous tissue collections left insufficient material for IHC testing Additional like deer samples for comparison were collected on both control farms as well as samples of water and feed.

The deer’s current ages are as follows - Red Buck 1, born on 6-4-15, genotype of 96/GS. Purple 1, born on 7-8-12, genotype 96/GS. Purple 2, 8-15-2019, 96/GS and Bull Elk 1, born 7-1-2009 with an unknown genotype.

Ultrasound examination noted that Purple 1 was undetermined to be pregnant though she was pregnant last year delivering her first fawn in 4 years time on August 15, 2019 after switching to the new test ration. If she was pregnant again she wasn’t showing it. This still provides a great opportunity to follow this doe with her first buck fawn (Purple 2) in the continued research efforts in the study of disease progression by the farming community. This fawn was born during the same timeframe that rectal positive Yellow 2 had her fawn last year but both had died by mid-August/September.



Top Left to Right – Red 1, Bull Elk 1. Bottom left to right Purple 1 and her buck fawn Purple 2 (8-15-2019) Body condition March 7, 2020. Purple 1 hair coat concern (left shoulder) turned out to be a louse infestation.

Samples

Sample collections from the deer and 1 Elk from the quarantine farm and control farms will examine the metabolic status of blood values and compare bacterial status for biological pathogen load. The bacterial reviews, in this phase of the research, will be provided with use of Quime 2 profiling tool for 16S RNA. Because of the complexity of DNA–DNA hybridization, 16S rRNA gene sequencing is used as a tool to identify bacteria at the species level and assist with differentiating between closely related bacterial species. This newer testing platform will provide a more in depth analysis by providing a more comprehensive review of RNA bacterial presence in relation to past sample results from the Quime 1 platform. The Quime 2 results are provided in a direct numerical number of enrichment vs. being presented as a percentage of detected bacterial. What this means is, in this report, data will be presented as a numerical number of enrichment, where, the higher the number, the more a bacteria are present. The same is true with a lower number showing less bacterial load. As we move through the data, this low number count should not be discounted since in the past reports, in this study, demonstrated that some low levels of bacteria detected in water were also found in deer’s’ saliva to brain tissues on the quarantine farm found positive for CWD (Phase 3.5).

Water samples will be collected from all 3 farms watering delivery systems that provide drinking water for deer on their respective farm. This expanded surveillance will help demonstrate, for other farmers, a comprehensive list of water-borne environmental bacteria which have the potential to cause disease across a geographical landscape. Since each of the 3 farms were on the same ration 1 feed sample will be acquired from the quarantine farm. This will allow for determination of bacterial organism shared in deer on the quarantine farm as compared to deer from each of the control farms via the nasal, saliva, blood and fecal sampling.

Results

The original water source on the quarantined farm had many gram negative bacteria in the well water testing. As an improvement, we replaced the piping from the artisanal well head that supplies the deer's' and 1 elk drinking water. This year, for the first time, the water testing from the well showed detection of acinetobacter bacteria but at a lower level on the quarantine farm as well as other control farms from across the state. Acinetobacter is a common environmental organism, but left undetected, is considered a group of organisms found to be antibiotic resistant. This was one of the major organisms found in Yellow 2, nose to brain regions, after succumbing to death and testing positive for CWD. Another new bacterial organism detected in one farm water was a mycobacterium group though at a lower rate of enrichment. Johne's disease is caused by Mycobacterium avian subspecies paratuberculosis, which belongs to the same family as tuberculosis and leprosy. (2) This particular organism type could be associated with the avian type of mycobacterium and has been linked to false positive TB results in deer. Independent research has also documented mycobacterium in samples of humic acid products used for land applied soil amendments. Other water born organisms of interest that were not present in the water samples this April were bacterial organisms such as Aeromonas, Shigella ecoli or mycoplasma in the farms' water source.

These past and current observations could be important for all cervid farms when considering water quality and feed and when reviewing geographic movements of cervids between farm pens in state or out of state. Proper water testing and water sanitation practices could play an important part in supporting animal health especially for long term holding facilities such as hunting ranches or purpose breeding facilities (Table 1).

In review of tables 1 – 11 in this report the respective identification of each farm and each farms associated water source will be connected to each farm respective deer (D = Doe / B = Buck) / Elk (key) that will be color coded at the top of each table (Blue = Control 1 Farm / Deer, Green = Control 2 Farm / Deer and Yellow = Quarantine Farm / Deer / Elk). This is important to follow throughout the report as to using this as a guide for similarities and differences found on different farms and in different sexes of different deer as compared along with Bull Elk 1.

Water / Feed Bacteria

Water Bacteria Associated with 3 Farm Supply	C Water 1	C Water 2	Q Water	Q Feed
Bacteroidetes; Bacteroides; uncultured bacterium	27	8	13818	0
Proteobacteria; Moraxellaceae; Psychrobacter	426	0	13148	0
Bacteroidetes; dgA-11 gut group; uncultured bacterium	0	0	5548	0
Proteobacteria; Conchiformibius	58	0	5056	0
Bacteroidetes; Prevotella 1	17	0	4963	0
Actinobacteria; Corynebacteriaceae	2304	199	3051	0
Tenericutes; Mollicutes RF39	258	0	2757	0
Bacteroidetes; Alistipes; uncultured bacterium	0	0	2710	0
Proteobacteria; Burkholderiaceae	97	0	2668	0
Bacteroidetes; Lacibacter; uncultured bacterium	0	0	2613	0
Firmicutes; Streptococcus; Ambiguous_taxa	60	777	2162	99
Firmicutes; Lachnospiraceae AC2044 group; uncul.bacterium	43	0	1288	0
Firmicutes; Christensenellaceae R-7 group	0	0	1284	0
Firmicutes; Ruminococcaceae UCG-013; uncul. bacterium	0	0	1251	127
Bacteroidetes; Barnesiella; uncultured bacterium	2312	0	1063	0
Verrucomicrobia; Akkermansia; uncultured bacterium	28	2074	150	0
Proteobacteria; Acinetobacter	372	4	107	0
Proteobacteria; Moraxellaceae; Moraxella	263	1743	0	0
Actinobacteria; Mycobacterium	37	0	0	0
Proteobacteria; Aeromonas	0	0	0	0
Proteobacteria; Escherichia-Shigella	0	0	0	0
Tenericutes; Mycoplasma	0	0	0	0

Table 1. Water / Feed bacteria most associated between control farm 1 (blue), control farm 2 (Green) and quarantine farm (Yellow) collected April 2020. Feed associated bacteria via sampling quarantine farm (purple).

Nasal Bacteria

Since the quarantine farm Doe population has been more prone to developing CWD, the nasal chart (Table 2) will compare bacterial organisms found in the water connection from deceased Yellow 2 who was confirmed with being CWD positive by NVSL. In using this comparison of identified organisms we will use the current results from Purple 1 Doe (Q Doe P1) from her “most” detected organism presence to the “least” organism detected. This could provide a more detailed way of review of what Doe deer on the quarantine farm have bacterially as compared to other Doe or buck deer on control farms. As noted from results, nasal bacterial detected in all deer / elk show a mix of bacterial organisms tied to respective farm waters and presence of common bacteria not associated with respective farm water. What is more important to note would be the bacterial organisms that are present in the deer / elk not associated with the respective farm water source. Nasal bacteria not associated with water sources on the respective farm shows a conserved set of organisms in deer and elk that could be unique to the respective farm or a geographic area. This could change at different stages of the deer’s lifetime or if moved to another farm location (Table 3). Nasal bacteria previously not found in water (Phase 3.5) source of the quarantine farm had organism enrichment counts such as Chryseobacterium (31753), Myroides (16727), Aeromonas (6842) and Acinetobacter (6749) as the top 4 nasal organisms present in the nasal samples of Yellow 2 whom was detected positive for CWD upon death. The current water source sampling from all farms show an associated environmental

organism found in deer with a positive CWD detection. This organism (acintobacter) was found in the nasal samples collected from all farms though at a lower rate than the water source. Though this finding was at a lower rate of enrichment it would still be considered a risk not to practice good water sanitation hygiene on the farms water delivery system for deer / elk.

Nasal Bacteria associated with Farm Water

Nasal Bacteria Associated with Farm Water	C Water 1	C Water 2	Q Water	C Doe 1	C Doe 2	Q Doe P1	C Buck 1	C Buck 2	Q Buck R1	Q Buck P2	Q Elk Bull1
Bacteroidetes; Bacteroides; uncul. bacterium	27	8	13818	18	0	0	50	0	78	0	46
Bacteroidetes; Prevotella 1	17	0	4963	288	0	0	1512	0	82	0	15
Firmicutes; Ruminococcus 2	199	0	959	0	0	105	150	0	199	63	158
Firmicutes; Family XIII; nodatum group; uncultured	18	0	290	67	0	117	175	0	47	30	0
Tenericutes; Anaeroplasma; uncultured bacterium	25	23	251	8	12	0	0	0	82	18	70
Firmicutes; Ruminococcaceae UCG-013; uncultured	97	0	146	34	0	35	0	8	52	0	43
Proteobacteria; Acinetobacter	372	4	107	85	0	29	82	0	58	64	55
Firmicutes; Clostridium sensu stricto 1	53	0	26	0	0	0	57	0	25	12	197
Firmicutes; Christensenellaceae R-7 group	100	0	17	0	0	42	57	0	0	0	134
Bacteroidetes; Alistipes; uncultured bacterium	64	0	17	181	0	28	150	0	16	40	15
Bacteroidetes; Petrimonas; uncul. bacterium	0	0	8	13	0	0	7	13	0	0	0
Firmicutes; Ruminococcaceae	20	0	6	0	0	14	0	0	24	0	85

Table 2. Nasal bacteria of found in deer / elk associated with farm water. Non-colored filled cells are bacterial organisms also present but were not associated with independent farm water.

Nasal Bacteria not associated with Farm Water

Nasal Bacteria NOT Associated with Farm Water	C Water 1	C Water 2	Q Water	C Doe 1	C Doe 2	Q Doe P1	C Buck 1	C Buck 2	Q Buck R1	Q Buck P2	Q Elk Bull1
Cyanobacteria; uncultured bacterium	0	0	0	127	0	7104	1564	5132	925	28152	0
Proteobacteria; Bibersteinia	0	0	0	497	0	4494	0	0	26364	34096	0
Proteobacteria; Alysia; Ambiguous taxa	0	0	0	0	18	2247	8837	0	625	5156	0
Proteobacteria; Psychrobacter	0	0	0	2537	39	709	2771	510	6036	26166	0
Firmicutes; uncultured Lachnospiraceae bacterium	45	0	0	7	1876	69	666	2	66	49	173
Firmicutes; Lachnospiraceae NK4A136 group	27	0	0	0	0	40	15	0	74	50	60
Bacteroidetes; Butyrivomax	0	0	0	0	0	27	0	3	25	45	0
Bacteroidetes; Rikenellaceae RC9 gut group	14	0	0	0	0	20	0	0	0	0	93
Bacteroidetes; Weeksellaceae	0	0	0	18	33190	6	159	0	92	0	0
Firmicutes; Streptococcus henryi	0	0	0	5	16185	5	85	0	58	0	0

Table 3. Nasal bacteria found in deer / elk not associated with respective farm water. Non-colored filled cells are bacterial organisms present but were not associated with independent farm water.

Saliva

Deer and elk saliva results show the same general bacterial sharing on all respective farms but with a more direct association to each respective farms water and feed. (Table 4)

When consuming water, feed or forages / hay in their daily routine deer / elk vary in most consumption across what is offered on a respective farm location. With this mixture of feedstuff saliva is consistently supplied in the oral cavity for the ruminants to ruminate aiding n digestion of the respective farms offerings. This makes saliva an important indicator of health assessment since it is the gateway of oral ingestion of nutrition for the deer / elk. In Phase 3.5, Yellow 2 (CWD+) was found to be exposed to water associated bacteria counts such as Escherichia – Shigella (2739), Streptococcus (2258) and Pseudomonas (1017) in her saliva sampling.

Escherichia – Shigella and Pseudomonas organisms were not found in the current water sources. Streptococcus and Acinetobacter were found in current farm water that were also present in current saliva samples.

Saliva Bacteria associated with Farm Water / Feed

Saliva Bacteria Associated with Farm Water/Feed	C Water 1	C Water 2	Q Water	Feed	C Doe 1	C Doe 2	Q Doe P1	C Buck 1	C Buck 2	Q Buck R1	Q Buck P2	Q Elk Bull1
Bacteroidetes; Bacteroides; uncultured bacterium	87	19316	13818	99	0	4	1394	0	2	4169	9838	138
Proteobacteria; Psychrobacter	426	0	13148	0	0	0	32	0	0	124	1734	0
Bacteroidetes; Rikenellaceae; dgA-11 gut group	0	920	5548	0	5	1789	8	13	0	1701	358	0
Proteobacteria; Conchiformibius	58	0	5056	0	0	0	0	728	8	0	0	0
Bacteroidetes; Prevotella; 1 uncultured bacterium	17	6886	4963	532	31	698	232	2366	223	1847	11196	1492
Proteobacteria; Burkholderiaceae; Ambiguous_taxa	130	7390	3162	53540	50	22038	279	64	1890	1097	839	4505
Bacteroidetes; Alistipes; uncultured bacterium	126	1134	2970	0	30	7	17	81	9	1213	350	735
Tenericutes; Mollicutes RF39	960	0	2714	558	0	30	43	5	86	160	527	69
Firmicutes; Streptococcus; Ambiguous_taxa	60	4470	2162	86198	106	6239	922	341	675	2314	3454	965
Firmicutes; Lachnospiraceae	1930	0	1698	532	179	686	225	2388	1472	863	2236	2583
Firmicutes; Christensenellaceae R-7 group	6264	5868	1284	638	1410	4038	6275	1376	177	4560	1937	3753
Bacteroidetes; Barnesiella; uncultured bacterium	2312	0	1063	0	16	0	0	0	0	0	12	0
Firmicutes; Ruminococcus 2	199	0	959	0	67	28	135	0	33	496	374	619
Bacteroidetes; Chryseobacterium	456	0	505	0	0	0	1581	0	0	850	598	0
Firmicutes; Ruminococcaceae NK4A214 group	1221	0	392	0	3193	3	2007	1627	74	2067	196	54
Spirochaetes; Treponema 2; uncultured bacterium	0	0	385	0	52	1241	17	401	1577	3505	156	14
Firmicutes; Clostridiales; Family XIII; nodatum group	18	0	290	0	16	0	26	0	141	39	34	0
Bacteroidetes; Bacteroidales; F082	0	0	280	142	0	538	105	7	0	1135	545	0
Tenericutes; Anaeroplasmia; uncultured bacterium	25	23	251	32	8	92	0	43	0	16	6	6
Firmicutes; Ruminococcaceae UCG-009; uncultured	1455	0	110	122	0	0	56	0	0	1218	101	43
Proteobacteria; Moraxellaceae; Acinetobacter	372	6	107	0	73	69	10	99	113	351	277	230
Bacteroidetes; Rikenellaceae RC9 gut group	74	5541	96	1151	0	405	286	0	60	1089	560	3348
Firmicutes; Clostridium sensu stricto 1	53	0	26	0	0	0	22	125	0	649	101	32
Firmicutes; Ruminococcaceae UCG-014	1058	9	9	0	0	276	4	1573	71	1616	470	130

Table 4. Saliva bacteria associated with farm water supply using quarantine water bacterial as “most” to “least” profile. Non-colored filled cells are bacteria present on respective farms but were not associated with independent farm water or feed.

In Phase 3.5, Yellow 2 had bacteria counts found in saliva that were not present in the quarantine farm water source upon testing. Phase 3.5 testing identified round bacterial organisms Myroides (35490), Aeromonas (10160), Comamonas (4538) and Bibersteinia (3160) that were still not found in current farm waters. Interesting and unexpected was finding of a K-9 associated fusobacteria taxon 345 and K-9 Bacterioidete: Capnocytophaga taxon 329 in the saliva samples of deer and elk. In checking for a potential source, it was noted the quarantine farm has allowed local dog groups to practice noise distraction training for service dogs in crowded public places. This could explain the feasibility that dog(s) presence with somehow an access to public feeding deer / elk or equipment / shared water sources could unknowingly provide this bacterium's to be transferred to deer / elk saliva.



Left to Right -- Purple 1 shows good mothering care of her fawn purple 3 (7-1-2020) at 21 days of age while Elk 1 basks in the mid July early morning sunshine.



Left to Right: Purple 2 born 8-15-2019 from Purple 1 (above) follows Red 1 (sire) to a shady spot in the heat of July sun. Red 1 has bred 5 different Does in past 4+ years where 4 are now deceased from CWD.

The quarantine farm provides water, feed and dry hay on a year round basis where as they receive no green-up forages grown in their pens during a normal growing season. This is due, in part, to the geographic area, which has high sandy soil porosity where forages would need irrigation to produce any quality type forages. Control farms in this study offer the same feed but supply different water and have the ability to provide different green up forages during the normal growing seasons. Dry hay-type forages are only provided on control farms during the non-growing season. By noting both water / feed associated saliva bacteria vs. non- associated bacteria show what the deer have as a core bacterial presence during rumination representing future exploration of rumen health via saliva (Table 5)

Saliva Bacteria not associated with Farm Water / Feed

Saliva Bacteria NOT Associated with Farm Water/Feed	C Doe 1	C Doe 2	Q Doe P1	C Buck 1	C Buck 2	Q Buck R1	Q Buck P2	Q Elk Bull1
Fusobacteria; Leptotrichia sp. K9 oral taxon 345	0	0	67953	0	0	0	90	44
Bacteroidetes; Weeksellaceae; Riemerella	0	0	9655	0	0	1991	9503	244
Bacteroidetes; Bacteroides thetaiotaomicron	746	0	2356	3521	0	84	1641	38
Firmicutes; Ruminococcaceae; Sporobacter	95	20	1370	0	1197	911	287	1000
Firmicutes; Ruminococcaceae UCG-013; uncultured	0	0	1271	0	0	0	0	0
Firmicutes; uncultured Veillonellaceae bacterium	0	0	472	0	6	129	98	445
Proteobacteria; Suttonella; uncultured bacterium	0	217	431	0	29	96	0	18
Proteobacteria; Sphingomonadaceae bacterium S16	0	5625	415	2642	396	26	0	0
Proteobacteria; Rickettsiales; Mitochondria	0	0	383	0	0	172	749	30
Bacteroidetes; Petrimonas; uncultured bacterium	0	0	264	0	0	248	917	62
Firmicutes; Erysipelotrichaceae; uncultured	0	0	206	0	0	0	0	0
Proteobacteria; Phenylbacterium	0	6	185	8	401	4087	1109	225
Firmicutes; Bacillus	0	0	173	0	0	62	0	2
Proteobacteria; Reyranella	3	26	151	0	0	5	0	2
Actinobacteria; Micrococccaceae	10	0	144	0	0	8	0	0
Proteobacteria; Porphyrobacter	0	0	125	0	8	33	0	809
Bacteroidetes; Butyricimonas	112	193	112	2560	38	241	1482	31
Deinococcus-Thermus; Deinococcus	85	0	110	409	17	1286	1143	13
Firmicutes; Ruminococcaceae UCG-002; uncultured	0	0	82	88	18	16	754	0
Proteobacteria; Novosphingobium	10	41	80	2	57	546	590	1086
Proteobacteria; Sphingomonas	0	14328	67	0	777	0	0	0
Bacteroidetes; metagenome	0	0	63	0	0	1612	70	0
Archaea; Methanobrevibacter	10	3691	49	0	1776	0	25	0
Archaea; Methanosphaera	0	0	32	0	0	143	489	59
Actinobacteria; Acidimicrobiia; uncultured	0	0	30	0	6	0	86	879
Actinobacteria; Brevibacterium	0	0	27	0	0	574	137	0
Actinobacteria; Cryobacterium	0	7	25	0	5	892	164	0
Actinobacteria; Rothia	15108	0	20	10	0	0	6	0
Actinobacteria; Atopobium; Ambiguous_taxa	0	133	20	11	98	0	0	0
Bacteroidetes; Prevotellaceae	0	0	18	0	0	151	0	1245
Bacteroidetes; Filobacterium	33	474	15	34	122	0	99	0
Bacteroidetes; Flavisolibacter	0	0	14	0	17	25	289	0
Bacteroidetes; Capnocytophaga sp. K-9 oral taxon 329	0	0	14	1853	0	0	0	3310
Bacteroidetes; Flavobacterium	0	0	11	0	0	3716	218	32
Bacteroidetes; Weeksellaceae; Bergeyella	0	13	7	0	14	198	18	2038

Table 5. Non-colored cells are saliva bacteria present but were not associated with independent farm water, feed supplied deer / elk.

Blood Values

Blood values for Doe deer collected in April show differences between Control farm 1 (normal range) and Control farm 2 and Quarantine farm (below Ref. Range). (Table 6) This could be important since these deer were determined to be pregnant. Above normal Creatine kinase levels could be due to excitement during the darting phase of sedation across different farms. This could have an impact on various blood values with deer / elk if blood is collected after being stressed during the capture phase whether using a handling chute vs. sedation. Extra samples were provided from control farms for supporting average values.

Metabolic Blood Values of Doe Deer

Blood Test	Unit	C1 Doe 1	C1 Doe 2	C1 Doe 3	C2 Doe 1	C2 Doe 2	C2 Doe 3	Q Doe P1	Doe avg.	Ref. Range
Total Protein	g/dL	6.1	5.7	5.7	6.2	5.6	4.8	5.2	5.6	5.0 - 7.8
Albumin	g/dL	3	3.2	3.1	2.8	2.8	3.4	3	3.04	2.5 - 4.2
Globulin	g/dL	3.1	2.5	2.6	3.4	2.8	1.4	2.2	2.57	1.0 - 4.0
Albumin: Globulin	Ratio	1	1.3	1.2	0.8	1	2.4	1.4	1.3	0.5-1.0
Glucose	mg/dL	340	180	186	177	120	138	183	189	60 - 320
Creatinine	mg/dL	1.4	1	0.9	0.9	1.4	1.1	1.5	1.17	0.4 - 2.0
BUN	mg/dL	23	34	35	22	31	20	33	28.2	7 - 35.0
Bilirubin - Total	mg/dL	0.4	0.7	0.9	0.5	1	<0.1	1.6	0.85	0.1 - 1.0
Cholesterol	mg/dL	59	52	45	64	77	98	nt	65.83	n/a
Calcium	mg/dL	8.1	8.5	8.6	7.1	6.2	7.2	7.7	7.6	8.8 - 10.8
Phosphorus	mg/dL	5	5.6	6.5	9.1	7.9	8.2	6.9	7	4.5 - 8.5
Magnesium	mg/dL	nt	nt	nt	2.3	1.8	2.3	2.1	2.1	n/a
Potassium	mmol/L	4.3	3.9	3.4	6.3	6.7	8.1	5.7	5.5	3.4 - 5.0
Sodium	mmol/L	145	144	145	143	144	143	136	142.8	132 - 156
Chloride	mmol/L	107	104	104	106	108	105	100	104.8	100 - 110
Na: K	Ratio	34	37	43	23	21	18	23.9	28.5	n/a
TCO2 (Bicarbonate)	mmol/L	21	26	26	20	18	24	nt	22.5	12 to 24
Anion Gap	mmol/L	21	18	18	23	25	22	nt	21.1	n/a
AST	U/L	73	94	173	85	71	85	89	95.7	40 - 150
GGT b	U/L	52	55	48	51	30	27	34	42.4	40 - 100
Creatine Kinase	U/L	453	279	1451	407	190	744	698	603	20 - 400
GLDH preg	U/L	nt	nt	nt	nt	nt	nt	15		n/a
BUN: Creatinine	Ratio	16	34	39	24.4	22.1	18.2	nt	25.6	n/a
V-NEFA		0.618	0.443	0.488	nt	nt	nt	0.6	0.53	0.2 - 0.8

Table 6. Blood values for Doe deer collected in April 2020. Collecting spring blood values help show overwintering condition of deer for considering any dietary adjustments.

Creatine kinase was above range in some Does but not the bucks / elk in collected samples across different farms (Table 7). Extra samples were provided from control farm 1 for supporting average values. Calcium values were more stable on buck / elk bloods vs. Doe bloods from each farm sampled. This may note that even with the same dietary feed input but different water / forages provided on all farms there may be a need to review Doe health during pregnancy with extra calcium support. This could also support fawn survivability if a farm is experiencing fawn loss in a given year that could be due to less than optimum Doe nutrition during pregnancy. NEFA values for both Doe / buck deer including the one bull elk were within satisfactory limits. High NEFA values would show a negative metabolic energy balance in ruminants supporting poor health (3)

Metabolic Blood Values of Buck Deer / Elk

Blood Test	Unit	C1 Buck 1	C1 Buck 2	C1 Buck 3	C2 Buck 1	Q Buck R 1	Q Buck P 2	Buck avg.	Ref. Range*	Q Bull Elk1
Total Protein	g/dL	5.3	5.6	5.4	5.3	6.4	5.4	5.56	5.0 - 7.8	5.9
Albumin	g/dL	3.1	3.2	3.2	3	3.2	3	3.11	2.5 - 4.2	3.4
Globulin	g/dL	2.2	2.4	2.2	2.3	3.2	2.4	2.45	1.0 - 4.0	2.5
Albumin: Globulin	Ratio	1.4	1.3	1.5	1.3	1	1.3	1.3	0.5-1.0	1.4
Glucose	mg/dL	160	193	209	232	111	158	177	60 - 320	94
Creatinine	mg/dL	0.7	1	0.9	0.8	1.2	0.9	0.92	0.4 - 2.0	2.6
BUN	mg/dL	25	34	32	15	33	29	28	7 - 35.0	26
Bilirubin - Total	mg/dL	0.1	1.3	0.6	0.3	1.1	1.3	0.78	0.1 - 1.0	0.2
Cholesterol	mg/dL	61	44	47	43	nt	nt	nt	n/a	nt
Calcium	mg/dL	9.8	8.8	9	8.6	8.5	9	8.95	8.8 - 10.8	9.4
Phosphorus	mg/dL	9.3	6.3	6.2	7	4.9	8.5	7.03	4.5 - 8.5	5.5
Magnesium	mg/dL	nt	nt	nt	1.9	2.1	1.8	1.93	n/a	2
Potassium	mmol/L	4.3	3.9	3.9	6.1	6.1	5.1	4.9	3.4 - 5.0	4.6
Sodium	mmol/L	148	143	142	143	136	136	141.3	132 - 156	145
Chloride	mmol/L	106	101	101	105	99	100	102	100 - 110	105
Na: K	Ratio	34	37	36	23	22.3	26.7	29.8	n/a	31.5
TCO2 (Bicarbonate)	mmol/L	27	27	27	24	nt	nt	26.25	12 to 24	nt
Anion Gap	mmol/L	19	19	18	20	nt	nt	19	n/a	nt
AST	U/L	73	106	169	94	103	115	110	40 - 150	38
GGT b	U/L	39	45	46	33	38	40	40.1	40 - 100	14
Creatine Kinase	U/L	133	306	292	197	457	227	268	20 - 400	99
BUN: Creatinine	Ratio	36	34	36	18.8	nt	nt	nt	n/a	nt
V-NEFA		0.044	0.614	0.231	nt	0.64	0.24	0.353	0.2-0.8	0.06

Table 7. Blood values for bucks in April 2020. *Reference range is for whitetail deer only.

Overall blood bacteria results were greatly reduced as a whole as compared to these deer from past results prior reports of this study (Table 8). Some of the water born bacteria that were not present as found in the past was Escherichia- Shigella, Mycobacterium and Aeromonas on the quarantine farm.

Blood Bacteria Associated with Farm Water

Blood Bacteria Associated with Farm Water	C Water 1	C Water 2	Q Water	C Doe 1	C Doe 2	Q Doe P1	C Buck 1	C Buck 2	Q Buck R1	Q Buck P2	Q Elk Bull1
Proteobacteria; Psychrobacter	426	0	13148	0	0	0	0	0	8	3	0
Proteobacteria; Conchiformibius	69	29786	5056	0	4	0	0	0	18	3	0
Firmicutes; Ruminococcus 2	199	0	959	0	0	0	0	0	23	20	0
Firmicutes; Family XIII AD3011 grp; uncul. rumen bacterium	0	0	250	0	0	0	0	0	3	0	0
Firmicutes; Ruminococcaceae UCG-013; uncul. bacterium	97	0	146	0	0	0	0	0	29	18	4
Cyanobacteria; Chloroplast	0	0	21	0	0	0	0	0	0	16	0
Bacteroidetes; Petrimonas; uncultured bacterium	0	0	8	13	0	0	0	4	21	38	0

Table 8. Blood bacteria associated with farm water supply. Non-colored filled cells are bacteria present that are not associated with independent farm water.

Bacteria organisms present in deer blood not associated with farm water/feed supply (Table 9). This was anticipated since all 3 farms were now being fed the same test feed designed for reduction in pro-inflammatory dietary compounds that could deter leaky gut syndrome. This overall reduction of blood bacteria points to a healthier blood profile of all deer / elk.

Blood Bacteria not associated with Farm Water

Blood Bacteria NOT Associated with Farm Water	C Water 1	C Water 2	Q Water	C Doe 1	C Doe 2	Q Doe P1	C Buck 1	C Buck 2	Q Buck R1	Q Buck P2	Q Elk Bull1
Firmicutes; Lachnospiraceae	0	0	0	0	0	156	0	0	2217	0	3
Bacteroidetes; Bacteroides; uncultured Bacteroides sp.	0	0	0	2058	879	63	3128	10480	0	0	157
Proteobacteria; Novosphingobium	173	0	0	0	0	0	0	0	21	18	0
Firmicutes; Christensenellaceae R-7 group	61	0	0	0	0	0	0	0	43	0	0
Proteobacteria; Brachymonas	15	0	0	0	2	0	0	0	25	0	0
Firmicutes; Ruminococcus 2; uncultured rumen bacterium	118	0	0	0	0	0	0	0	13	0	0
Firmicutes; Ruminococcaceae	0	0	0	1117	0	0	0	0	0	0	0
Firmicutes; Lachnospiraceae UCG-010; uncul. bacterium	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria; Escherichia-Shigella	0	0	0	0	0	0	0	0	0	0	0
Actinobacteria; Mycobacterium	0	0	0	0	0	0	0	0	0	0	0
Proteobacteria; Aeromonas	0	0	0	0	0	0	0	0	0	0	0

Table 9. Blood bacteria NOT associated with farm water supply. Non-colored filled cells are bacteria present that are not associated with independent farm water.

In the past, Yellow 2 had bacterial counts for *Clostridium sensu stricto* 11 (8) and *Mycoplasma: erthrocerve* (7) found in blood samples not associated with the farm water. Water supply from the quarantine farm is presented in a most to least value of sample enrichment for comparison of fecal samples collected from each farm (Table 10). The only common environmental organism, acinetobacter, was found associated with each farm water supplies. Though at a lower rate of enrichment in water, this bacteria shows a higher rate of enrichment in fecal samples tested of deer but not elk. This demonstrates that this common organism in the environment is consumed from a detected water source transits through the animal to fecal content. This could be a normal course of a digestive system ridding itself of pathogenic bacteria. The concern would be if a deer / elk develop an acute or chronic pro-inflammatory condition due to an illness or improper dietary intake. Left untreated these illness / nutritional conditions could lead to a leaky gut syndrome condition allowing these types of negative associated organisms to enter the areas of the body where they do not belong. This, in turn, will degrade the deer / elk health condition to a point of metabolic dysfunction and or death.

Fecal Bacteria associated with Farm Water / Feed

Fecal Bacteria Associated with Farm Water / Feed	C Water 1	C Water 2	Q Water	Feed	C Doe 1	C Doe 2	Q Doe P1	C Buck 1	C Buck 2	Q Buck R1	Q Buck P2	Q Elk Bull1
Proteobacteria; Neisseriaceae; Conchiformibius	58	0	5056	0	0	0	0	0	0	0	0	5
Actinobacteria; Corynebacteriaceae	2304	199	3051	0	0	0	0	0	0	0	4	0
Firmicutes; Clostridia; Ruminococcus 2	199	0	959	0	0	0	20	0	0	27	28	110
Proteobacteria; Burkholderiaceae	0	0	494	23	0	0	15	0	0	0	0	29
Bacteroidetes; Bacteroidales; F082	0	0	188	0	2	0	0	0	0	0	0	9
Proteobacteria; Moraxellaceae; Acinetobacter	372	4	107	127	2098	320	1081	3027	1400	880	705	63
Firmicutes; Clostridia; coprostanoligenes group; uncul. bacterium	0	0	87	0	0	0	0	0	0	4	0	0
Firmicutes; Clostridia; Christensenellaceae	37	0	42	0	0	0	0	0	0	0	20	0
Firmicutes; Clostridia; Defluviitaleaceae UCG-011; uncul. bacterium	0	0	30	0	0	0	4	0	0	0	0	0
Firmicutes; Bacilli; Streptococcus	0	0	26	27	0	0	0	3	0	0	0	0
Firmicutes; Clostridia; Clostridium sensu stricto 1	53	0	26	0	143	0	22	58	0	19	373	1348
Actinobacteria; Microbacteriaceae; Leucobacter	0	0	17	0	0	0	0	0	0	0	0	7
Bacteroidetes; Alistipes; uncultured bacterium	15	0	17	0	4	0	13	0	0	5	60	510
Firmicutes; Clostridia; Christensenellaceae R-7 group	44	0	17	0	361	0	43	176	0	24	458	1121
Firmicutes; Bacilli; Staphylococcus	0	0	16	0	0	0	0	0	0	0	0	0
Proteobacteria; Brevundimonas diminuta	0	0	14	0	0	0	0	0	0	0	0	6
Firmicutes; Clostridia; coprostanoligenes group	13	0	10	0	0	0	0	0	0	10	5	20
Firmicutes; Clostridia; Ruminococcaceae UCG-014	26	9	9	0	0	0	0	10	0	0	0	0
Firmicutes; Clostridia; Ruminococcaceae UCG-005; uncul. bacterium	0	0	5	0	0	0	0	0	0	0	0	9
Proteobacteria; Moraxellaceae; Psychrobacter	0	0	4	0	0	0	0	0	0	0	207	0
Bacteroidetes; Spirosomaceae; Emticicia	0	0	3	0	22	0	0	190	4	0	0	0
Firmicutes; Clostridia; Lachnospiraceae UCG-010; uncul. bacterium	0	0	3	0	0	0	0	0	0	0	0	0
Firmicutes; Erysipelotrichia; Turicibacter	0	0	3	0	186	20	396	136	11	135	186	0
Firmicutes; Clostridia; Lachnospiraceae NK4B4 grp; uncul. bacterium	0	0	2	0	0	0	0	260	0	0	0	0
Proteobacteria; Arenimonas	0	0	2	0	231	0	0	2836	185	0	0	0
Proteobacteria; Solimonadaceae; Nevskia; Ambiguous_taxa	0	0	2	0	186	0	83	0	64	0	41	7

Table 10. Fecal bacteria associated with farm water/feed supplied to deer/elk. Non-colored cells are bacteria present that are not associated with independent farm water.

Bacteria not associated with water or feed shows the uniqueness of each farm deer / elk base organisms detected in April 2020. At the time that Yellow 1 had passed (Phase 3.5) the water had a bacterial count for Escherichia-Shigella of 4 whereas her fecal sample detected a count of 3600. Other bacterial organisms she had onboard, not found in water samples, was Acinetobacter lwoffii (2398) and Fusobacterium (2048). Other areas of bacteria cross contamination on a farm for non- water associated contamination not reviewed would be from rodents / birds. Rodents / birds can contribute to the spread of disease. For example, if rodents / birds are attracted to feed, and feed contaminated by fecal matter can serve as a source of pathogens. Therefore, this would be an important part of farm bio-security (4) for deer / elk.

Fecal Bacteria not associated with Farm Water / Feed

Fecal Bacteria NOT Associated with Farm Water / Feed	C Doe 1	C Doe 2	Q Doe P1	C Buck 1	C Buck 2	Q Buck R1	Q Buck P2	Q Elk Bull1
Tenericutes; Mollicutes; Mycoplasma haemocervae	1589	323	4449	1049	254	1386	2469	2895
Cyanobacteria; Chloroplast	93	0	2896	191	28	361	3807	167
Proteobacteria; Burkholderiaceae; Brachymonas	1215	165	2742	813	144	2167	3895	1945
Firmicutes; Bacilli; Streptococcus	1034	0	2220	2483	614	1214	2825	219
Bacteroidetes; Bacteroides; uncultured bacterium	1931	372	2154	3247	3750	1790	2156	2906
Bacteroidetes; Rikenellaceae RC9 gut group; uncultured	0	480	1784	64	55	1063	7587	264
Firmicutes; Clostridia; Ruminococcaceae UCG-002;uncultured	377	0	1681	301	23	2011	967	140
Proteobacteria; Burkholderiaceae; Pelistega	2141	988	1563	1865	1088	2371	1115	256
Firmicutes; Clostridia; Ruminococcaceae UCG-014	0	0	1485	0	0	9	0	0
Fusobacteria; Leptotrichia sp. canine oral taxon 345	59	0	1435	19	138	1652	511	0
Firmicutes; Clostridia; Christensenellaceae R-7 group	156	16	1430	249	352	691	490	3366
Firmicutes; Erysipelotrichia; Erysipelatoclostridium	82	0	1211	0	0	2788	1078	37
Firmicutes; Clostridia; Lachnospiraceae	503	0	805	428	47	749	443	901
Proteobacteria; Burkholderiaceae; Delftia	119	0	652	47	70	260	976	0
Bacteroidetes; p-251-o5; uncultured bacterium	736	48	480	417	698	189	656	2388
Firmicutes; Bacilli; Streptococcus sp. C819	869	0	425	634	16	527	192	1392
Firmicutes; Clostridia; Romboutsia	889	192	375	316	326	82	0	0
Bacteroidetes; Weeksellaceae; Bergeyella	867	95	348	1002	2896	344	298	0
WPS-2; Ambiguous_taxa	20	0	327	51	111	858	196	536
Proteobacteria; Moraxellaceae; Psychrobacter	607	0	282	2245	1093	771	920	0
Bacteroidetes; Sphingobacteriaceae	1233	116	271	539	2681	499	1077	0
Bacteroidetes; Chitinophagaceae; Sediminibacterium	86	0	255	39	0	0	2597	0
Bacteroidetes; Prevotella 1; uncultured rumen bacterium	39	0	125	180	151	0	0	817
Proteobacteria; Cardiobacteriaceae; Suttonella	1122	0	26	1194	306	417	54	20
Proteobacteria; Cellvibrionaceae; Cellvibrio	0	943	22	0	0	0	0	0
Proteobacteria; Rhodobacter; uncultured bacterium	2321	0	2	171	3738	0	0	0
Bacteroidetes; Muribaculaceae; uncultured bacterium	0	0	0	0	0	0	613	574
Firmicutes; Clostridia; Ruminococcaceae NK4A214 group	0	353	0	0	0	0	0	35
Tenericutes; Anaeroplasma; uncultured bacterium	0	0	0	0	0	0	0	1233

Table 11. Fecal bacteria not associated with respective farm water/feed supply.

Summary of findings

In summary, samples were collected for determining current health assessments of deer and elk between control farms and a quarantine farm for determining Chronic Wasting Disease origins. Drinking water and feed samples were taken from the 3 respective farms for along with nasal, oral, blood and feces of each deer and elk in the study. Current identified bacterial organisms were further defined as to association with or without a connection to the animals' water or feed source or deer / elk bacterial base content not associated to feed or water. This year's bacterial profile shows a continued positive health effect as compared to past negatively associated bacterial organisms in deer and elk. Purple 1 provided a second buck fawn this year showing continued positive direction for re-establishment of reproduction. Though there were positive associated organisms present in deer there were also newly found negative associated organisms for the first time in the respective water supply of each farm. Review of additional blood markers pertaining to the metabolic health status provided a continued basis of the deer / elk for overall health at this time point in the spring collection of samples.



Doe Purple 1 (7-8-2012) good body condition in November post birthing Purple 3 born 7-1 2020.



Buck, Red 1 (6-4-15) with Purple 2 born 8-15-2019 showing good body condition mid November.



Approaching 5 years of CWD quarantine January 2021, Bull Elk 1 adds body weight for the winter months.

Discussion

In review of the overall study this year, samples collected and submitted in April 2020 were delayed for processing due to Covid-19 redirection of testing resources in multiple Academic Institutions for this human associated pandemic concern.

This spring, we continued the assessment of our quarantine farm along with deer from 2 control farms in different geographical areas in non-CWD areas of the state of Wisconsin. This assessment is to determine what is normally physiologically-associated with control farm deer health as compared to differences found with farmed deer / elk held under quarantined conditions for CWD. We do have to proceed with remembering that deer / elk on the quarantine farm have had prior exposure to negative bacteria diminishing their respective immune function. The deer have also been exposed multiple times to other deer deceased with CWD being detected upon death. Move forward, past our original 5th year of initial CWD exposure (Jan.2021), we hope to show benefits of these health improvements to diminish deer / elk developing CWD.

Deer on control and quarantine farms continue to show values of bacterial likeness being fed the same feed pellet. More importantly, it starts to show true differences between each farm deer associated with their respective farm water and other forage sources fed deer / elk and shows core bacterial organisms not associated with water / feed in deer / elk.

For the first time we found *Acinetobacter* being detected in water sources though at a low level. This level was noted to be found highest in the deer but not elk fecal material and to a lesser extent in their respective saliva samples. This organism is of concern because of associated antibiotic resistance if it gains a foothold in deer / elk. This organism could be eliminated from the deer / elk water source by proper water sanitation practices for potable water.

One good change found on the quarantine farm this year was the reduction / elimination of undesirable organisms like *Escherichia – Shigella* and *mycoplasma* from the deer's' blood. *Aeromonas* and *Myroides* were also found to be present in past water testing and deer samples on the quarantine farm that were also absent in this years assessments. The absence of these negative health-associated organisms in quarantine deer is a welcome finding. Past samplings of

blood from the quarantine farm, that contained these negative associated bacteria, were associated with deceased deer later determined positive with CWD. Overall, quarantine deer / elk continue to show higher levels of bacterial enrichments than control farms overall.

It is unknown the geographical distribution of negative associated bacterial organisms in the environment. Keeping them off of your farm is the biggest challenge farming faces in today's production cycles given they arrive to your farm be it wind, rain, bird, vermin or predator. What we can control is untreated water since this can be a tremendous source of negative associated bacterial in deer / elk. Be it water from a pond, creek, river or lake it is still an untreated source of drinking water. Here in Wisconsin, as well as in other states, surface water sources or shallow wells (sand points) are of concern since water supply systems from private wells are un-regulated in part (5).

When a water source is not treated in some manner it would be considered a non-potable water source. Not maintaining potable water (clean/fresh) sources for deer / elk exposes them unnecessarily to risks that could lead to an undesirable outcome in farm production. Deeper drilled water wells are regulated but still have a need for monitoring and routine bacterial sanitation maintenance. This is why in larger towns and cities treat water sources for human consumption, in some manner, to mitigate negative associated bacteria and health concerns. Farmers should view this information and take appropriate action for their own livestock support of production.

Some other reference recommendations for reducing the potential spread of Chronic Wasting Disease (6) would be worth building or adding to your farm bio-security plan. It is noted that any artificial water structures are one of the most common vehicles for environmentally transmitted diseases (7). Although prion molecules are hydrophobic, and cannot exist freely in water, they exist bound to particulate and organic matter in aquatic environments (8). Organic matter in water troughs allows for increased prion accumulation if present and the potential for prolonged infectivity compared to clean water sources (9). Artificial water structures, such as water troughs and guzzlers, placed on the landscape, whether for agricultural purposes or specifically for wild animals, are accessed by deer. These water structures can repeatedly attract deer at concentrated sites (10), allowing for increased contact between animals and the potential for disease transmission (11) between wild deer and domestic livestock. Increased prion accumulation in water containing organic particulates, and increased contact rates associated with artificial water structures pose the potential risk of CWD transmission among deer.

Some general recommendation / practices to reduce potential disease transmission at artificial water structures:

- a. Place water structure in locations undesirable or inaccessible to wild deer
- b. Keep water clean of organic matter and particulates
- c. Replace water frequently
- d. Frequently clean water structure with a 50:50 bleach water solution
- e. Avoid the use of stainless steel and porous materials for construction of water containment structures
- f. Do not intentionally place water structure on the landscape for wild deer

As we continue to learn the bacterial status and their respective differences on each farm in the study it's apparent that the farmed deer under quarantine for CWD still had a higher negative

organism composition than the deer of the control farms. An increased and sustained level of a negative associated bacteria load is what diminishes a deer's immunity status. Continued negative associated bacteria load in deer / elk could also have a negative health impact of reproduction, survivability and or products to market.

Besides water sources it is important when sourcing feeds including supplements' or trace minerals for nutritional inputs of deer/ elk to ensure these items are tested to quantify their appropriateness before providing to deer/elk. This review of dietary inputs would provide the deer the opportunity to perform to a healthier production status.

By reviewing 3 different rations on 3 different farms in the beginning we decided to change the base feed inputs on the 3 farms to the same pellet ration. This test ration being fed on all 3 farms has currently provided for a healthier profile to deer/elk providing more consistent results across each farm. This provides for the opportunity to measure and follow identified healthier markers in deer on control farms from the improvement of the nutritional inputs. These improvements to date have shown a reduction in negative associated organisms identified in past deer samples allowing for refinement in this research review. This change from negative to a more positive associated organism expression should provide support to the deer's immune system to perform at more normal rate. This in turn would minimize the opportunity of negative environmental organisms to create negative conditions in your deer / elk.

In mammalian species it is noted that aging is considered the main risk factor for several neurodegenerative diseases and is accompanied by chronic altered inflammation involving changes in microglial morphology, phenotype and activity (12). By developing and implementing a sound feeding and bio-security program for your farm will support your core farming activities (fawn / calf production) for the products of future sales. While noting and minimizing the risk factors for developing chronic inflammation we have delineated in this research review to date provides a path forward to achieve positive farm production goals.

I appreciate the opportunity to provide this information to the industry and look forward to the pending updates from this Phase 4 study installment in a follow up of these deer/ elk in a proposed Phase 5.

You the member, hold the key in supporting this continued research. Your input is highly valued. **Contact your Industry Leaders to have a conversation supporting CWD research.**

WCDEFA, wcdafa@gmail.com , NADeFA schafer@nadefa.org , or DBC cati@dbcdeer.com.

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